

01/07

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RAW SEQUENCE LISTING

DATE: 01/30/2002

PATENT APPLICATION: US/09/991,681

TIME: 17:26:06

Input Set : N:\Crf3\RULE60\09991681.txt

Output Set: N:\CRF3\01302002\I991681.raw

SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BILLING-MEDEL, PATRICIA
 7 COHEN, MAURICE
 8 COLPITTS, TRACEY L.
 9 FRIEDMAN, PAULA N.
 10 GORDON, JULIAN
 11 GRANADOS, EDWARD N.
 12 HODGES, STEVEN C.
 13 KLASS, MICHAEL R.
 14 KRATOCHVIL, JON D.
 15 ROBERTS-RAPP, LISA
 W--> 16 RUSSELL, JOHN C.
 W--> 17 STROUPE, STEPHEN D.

C--> 19 (ii) TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
 20 FOR DETECTING DISEASES OF THE PROSTATE

22 (iii) NUMBER OF SEQUENCES: 33

24 (iv) CORRESPONDENCE ADDRESS:

25 (A) ADDRESSEE: Abbott Laboratories
 26 (B) STREET: 100 Abbott Park Road
 27 (C) CITY: Abbott Park
 28 (D) STATE: IL
 29 (E) COUNTRY: USA
 30 (F) ZIP: 60064-3500

32 (v) COMPUTER READABLE FORM:

33 (A) MEDIUM TYPE: Diskette
 34 (B) COMPUTER: IBM Compatible
 35 (C) OPERATING SYSTEM: DOS
 36 (D) SOFTWARE: FastSEQ for Windows Version 2.0

38 (vi) CURRENT APPLICATION DATA:

C--> 39 (A) APPLICATION NUMBER: US/09/991,681

C--> 40 (B) FILING DATE: 26-Nov-2001

41 (C) CLASSIFICATION:

43 (vii) PRIOR APPLICATION DATA:

44 (A) APPLICATION NUMBER: 09/065,383

45 (B) FILING DATE:

49 (viii) ATTORNEY/AGENT INFORMATION:

50 (A) NAME: Becker, Cheryl L.

51 (B) REGISTRATION NUMBER: 35,441

52 (C) REFERENCE/DOCKET NUMBER: 6084.US.P1

54 (ix) TELECOMMUNICATION INFORMATION:

55 (A) TELEPHONE: 847/935-1729

56 (B) TELEFAX: 847/938-2623

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57      (C) TELEX:
62 (2) INFORMATION FOR SEQ ID NO: 1:
64      (i) SEQUENCE CHARACTERISTICS:
65          (A) LENGTH: 232 base pairs
66          (B) TYPE: nucleic acid
67          (C) STRANDEDNESS: single
68          (D) TOPOLOGY: linear
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73      GGCGCATCCG AGCCATGGCC CAGCAGGTGT TTATGCTGGA CACCCAGTGC TCACCAAAGA      60
74      CACCAAACAA CTTTGACCAC GCTCAGTCTT GCCAGTCTAT TATTGAGCTG CCTCCTGATG      120
75      AAAAACCAAA TGGACACACC AAGAAAAGCG TGTCTTTCAG GGAAATTGTG GTGAGCCTGC      180
76      TGTCTCATCA GGTGTTACTC CAGAACTTAT ATGACATCTT GTTAGAAGAG TT      232
78 (2) INFORMATION FOR SEQ ID NO: 2:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 289 base pairs
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: single
84          (D) TOPOLOGY: linear
87      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
89      CTTTCAGGGA AATTGTGGTG AGCCTGCTGT CTCATCAGGT GTTACTCCAG AACTTATATG      60
90      ACATCTTGTT AGAAGAGTTT GTCAAAGGCC CCTCTCCTGG AGAGGAAAAG ACGATACAAG      120
91      TGCCAGAAGC CAAGCTGGCT GGCTTCCTCA GATACATCTC TATGCAGAAC TTGGCAGTCA      180
92      TATTGACCTT GCTGCTGGAC TCTTATAGGA CTGCCAGGGA GTTTGACACC AGCCCCGGGC      240
93      TGAAGTGCCT GCTGAAGAAA GTGTCTGGCA TCGGGGGCGC CGCCAACCT      289
95 (2) INFORMATION FOR SEQ ID NO: 3:
97      (i) SEQUENCE CHARACTERISTICS:
98          (A) LENGTH: 264 base pairs
99          (B) TYPE: nucleic acid
100          (C) STRANDEDNESS: single
101          (D) TOPOLOGY: linear
104      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
106      GGCAGTCATA TTCGACCTGC TGCTGGACTC TTATAGGACT GCCAGGGAGT TTGACACCAG      60
107      CCCCAGGCTG AAGTGCCTGC TGAAGAAAGT GTCTGGCATC GGGGGCGCCG CCAACCTCTA      120
108      CCGCCAGTCT GCGATGAGTT TAACATTTAT TTCCACGCCC TGGTGTGTGC TGTTCTCACC      180
109      AATCAAGAAA ACATCACGGC CGAGCAAGTG AAGAAGGTCC TTTTGTGAGGA CGACGAGAGA      240
110      AGCACGGATT CTTCCAGCA GTGT      264
112 (2) INFORMATION FOR SEQ ID NO: 4:
114      (i) SEQUENCE CHARACTERISTICS:
115          (A) LENGTH: 260 base pairs
116          (B) TYPE: nucleic acid
117          (C) STRANDEDNESS: single
118          (D) TOPOLOGY: linear
121      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
123      CATATTCGAC CTGCTGCTGG ACTCTTATAG GACTGCCAGG GAGTTTGACA CCAGCCCCGG      60
124      GCTGAAGTGC CTGCTGAAGA AAGTGTCTGG CATCGGGGGC GCCGCCAACC TCTACCGCCA      120
125      GTCTGCGATG AGCTTTAACA TTTATTTCCA CGCCCTGGTG TGTGCTGTTC TCACCAATCA      180
126      AGAAACCATC ACGGCCGAGC AAGTGAAGAA GGTCCTTTTT GAGGACGACG AGAGAAGCAC      240
127      GGATTCTTCC CAGCAGTGTT      260
129 (2) INFORMATION FOR SEQ ID NO: 5:

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131      (i) SEQUENCE CHARACTERISTICS:
132          (A) LENGTH: 199 base pairs
133          (B) TYPE: nucleic acid
134          (C) STRANDEDNESS: single
135          (D) TOPOLOGY: linear
138      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
140      CCACTGGGTC CCAGGGGCCA GGACTCCCCG CTGCTTCAGC GTCCCCAGCA CTTGATGGAC      60
141      CAAGGGCAAA TCGGCATTTC CTTAGCGCA GGCCCCGAGC TGCTGCGACA GGACAAGAGG      120
142      CCCCCTCAG GCTCCACCGG GAGCTCCCTC AGTGCTCGG TGAGAGACGC AGAAGCACAG      180
143      ATCAGGCATG GACCAACAT      199
145 (2) INFORMATION FOR SEQ ID NO: 6:
147      (i) SEQUENCE CHARACTERISTICS:
148          (A) LENGTH: 470 base pairs
149          (B) TYPE: nucleic acid
150          (C) STRANDEDNESS: single
151          (D) TOPOLOGY: linear
154      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
156      CATTCCTTCA GCGCAGGCC CGAGCTGCTG CGACAGGACA AGAGGCCCG CTCAGGCTCC      60
157      ACCGGGAGCT CCCTCAGTGT CTCGGTGAGA GACGCAGAAG CACAGATCCA GGCATGGACC      120
158      AACATGGTGC TAACAGTTCT CAATCAGATT CAGATTCTCC CAGACCAGAC CTTACGGCC      180
159      CTCCAGCCCG CAGTGTTCCC GTGCATCAGT CAGCTGACCT GTCACGTGAC CGACATCAGA      240
160      GTTCGCCAGG CTGCGAGGGA GTGGCTGGGC AGGGTGGGCC GTGTCTATGA CATCATTTGT      300
161      TAGCCGACTC CTGTTCTACT CTCCCACCAA ATAACAGTAG TGAGGGTTAG AGTCCTGCCA      360
162      ATACAGCTGT TGCATTTTCC CCACCACTAG CCCCCTTAA ACTACTACTA CTGTCTCAGA      420
163      GAACAGTGTT TCCTAATGTA AAAAGCCTTT CCAACCACTG ATCAGCATTA      470
165 (2) INFORMATION FOR SEQ ID NO: 7:
167      (i) SEQUENCE CHARACTERISTICS:
168          (A) LENGTH: 232 base pairs
169          (B) TYPE: nucleic acid
170          (C) STRANDEDNESS: single
171          (D) TOPOLOGY: linear
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
176      CACGGCCCTC CAGCCCGCAG TGTTCCCGTG CATCAGTCAG CTGACCTGTC ACGTGACCGA      60
177      CATCAGAGTT CGCCAGGCTG TGAGGGAGTG GCTGGGCAGG GTGGGCCGTG TCTATGACAT      120
178      CATTGTGTAG CCGACTCCTG TTCTACTCTC CCACCAAATA ACAGTAGTGA GGGTTAGAGT      180
179      CCTGCCAATA CAGCTGTTGC ATTTTCCCCA CCACTAGCCC CACTTAACT AC      232
181 (2) INFORMATION FOR SEQ ID NO: 8:
183      (i) SEQUENCE CHARACTERISTICS:
184          (A) LENGTH: 244 base pairs
185          (B) TYPE: nucleic acid
186          (C) STRANDEDNESS: single
187          (D) TOPOLOGY: linear
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
192      TAAGGTTTGT ATCTAGATGA CACAAACGAT ATTCTGATTT TGCACATTAT TATAGAAGAA      60
193      TCTATAATCC TTGATATGTT TCTAACTCTT GAAGTATATT TCCCAGTGCT TTTGCTTACA      120
194      GTGTTGTCCC CAAATGGGTC ATTTTCAAGG ATTACTCATT TGAAAACACT ATATTGATCC      180
195      ATTTGATCCA TCATTTAAAA AATAAATACA ATTCTAAGG CAATATCTGC TGGTAAGTCA      240
196      AGCT
198 (2) INFORMATION FOR SEQ ID NO: 9:

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200 (i) SEQUENCE CHARACTERISTICS:
201 (A) LENGTH: 1771 base pairs
202 (B) TYPE: nucleic acid
203 (C) STRANDEDNESS: single
204 (D) TOPOLOGY: linear
207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
209 GGCAGTCATA TTCGACCTGC TGCTGGACTC TTATAGGACT GCCAGGGAGT TTGACACCAG 60
210 CCCCAGGCTG AAGTGCCTGC TGAAGAAAGT GTCTGGCATC GGGGGCGCCG CCAACCTCTA 120
211 CCGCCAGTCT GCGATGAGCT TTAACATTTA TTCCACGCC CTGGTGTGTG CTGTTCTCAC 180
212 CAATCAAGAA ACCATCACGG CCGAGCAAGT GAAGAAGGTC CTTTTGAGG ACGACGAGAG 240
213 AAGCACGGAT TCTTCCAGC AGTGTTTCATC TGAGGATGAA GACATCTTTG AGGAAACCGC 300
214 CCAGGTCAGC CCCCAGAGAG GCAAGGAGAA GAGACAGTGG CGGGCACGGA TGCCCTTGCT 360
215 CAGCGTCCAG CCTGTCAGCA ACGCAGATTG GGTGTGGCTG GTCAAGAGGC TGCACAAGCT 420
216 GTGCATGGAA CTGTGCAACA ACTACATCCA GATGCACTTG GACCTGGAGA ACTGTATGGA 480
217 GGAGCCTCCC ATCTTCAAGG GCGACCCGTT CTTCATCCTG CCCTCCTTCC AGTCCGAGTC 540
218 ATCCACCCCA TCCACCGGGG GCTTCTCTGG GAAAGAAACC CCTCCGAGG ATGACAGAAG 600
219 CCAGTCCCGG GAGCACATGG GCGAGTCCCT GAGCCTGAAG GCCGGTGGTG GGGACCTGCT 660
220 GATGCCCCCC AGCCCCAAAG TGGAGAAGAA GGATCCCAGC CGGAAGAAGG AGTGGTGGGA 720
221 GAATGCGGGG AACAAAATCT ACACCATGGC AGCCGACAAG ACCATTTCAA AGTTGATGAC 780
222 CGAATACAAA AAGAGGAAAC AGCAGCACAA CCTGTCCGCG TTCCCCAAAG AGGTCAAAGT 840
223 GGAGAAGAAA GGAGAGCCAC TGGGTCCCAG GGGCCAGGAC TCCCCGCTGC TTCAGCGTCC 900
224 CCAGCACTTG ATGGACCAAG GGCAAATGCG GCATTCTTC AGCGCAGGCC CCGAGCTGCT 960
225 GCGACAGGAC AAGAGGCCCC GCTCAGGCTC CACCGGGAGC TCCCTCAGTG TCTCGTGAG 1020
226 AGACGCAGAA GCACAGATCC AGGCATGGAC CAACATGGTG CTAACAGTTC TCAATCAGAT 1080
227 TCAGATTCTC CCAGACCAGA CCTTCACGGC CCTCCAGCCC GCAGTGTTC CGTGCAATCAG 1140
228 TCAGCTGACC TGTCACGTGA CCGACATCAG AGTTCGCCAG GCTGTGAGGG AGTGGCTGGG 1200
229 CAGGGTGGGC CGTGTCTATG ACATCATTGT GTAGCCGACT CCTGTTCTAC TCTCCCACCA 1260
230 AATAACAGTA GTGAGGGTTA GAGTCCTGCC AATACAGCTG TTGCATTTTC CCCACCACTA 1320
231 GCCCCACTTA AACTACTACT ACTGTCTCAG AGAACAGTGT TTCCTAATGT AAAAAGCCTT 1380
232 TCCAACCACT GATCAGCATT GGGGCCATAC TAAGGTTTGT ATCTAGATGA CACAAACGAT 1440
233 ATTCTGATTT TGCACATTAT TATAGAAGAA TCTATAATCC TTGATATGTT TCTAACTTT 1500
234 GAAGTATATT TCCAGTGCT TTTGCTTACA GTGTTGTCCC CAAATGGGTC ATTTTCAAGG 1560
235 ATTACTCATT TGAAAACACT ATATTGATCC ATTTGATCCA TCATTTAAAA AATAAATACA 1620
236 ATTCCTAAGG CAATATCTGC TGGTAAGTCA AGCTGATAAA CACTCAGACA TCTAGTACCA 1680
237 GGGATTATTA ATTGGAGGAA GATTTATGGT TATGGGTCTG GCTGGGAAGA AGACAACATAT 1740
238 AAATACATAT TCTTGGGTGT CATAATCAAG A 1771
240 (2) INFORMATION FOR SEQ ID NO: 10:
242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 2096 base pairs
244 (B) TYPE: nucleic acid
245 (C) STRANDEDNESS: single
246 (D) TOPOLOGY: linear
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
251 GGCGCATCCG AGCCATGGCC CAGCAGGTGT TTATGCTGGA CACCCAGTGC TCACCAAAGA 60
252 CACCAAACAA CTTTGACCAC GCTCAGTCCT GCCAGTCAT TATTGAGCTG CCTCCTGATG 120
253 AAAAACCAAA TGGACACACC AAGAAAAGCG TGTCTTTTCAG GGAAATTGTG GTGAGCCTGC 180
254 TGTCTCATCA GGTGTTACTC CAGAACTTAT ATGACATCTT GTTAGAAGAG TTTGTCAAAG 240
255 GCCCCTCTCC TGGAGAGGAA AAGACGATAC AAGTGCCAGA AGCCAAGCTG GCTGGCTTCC 300
256 TCAGATACAT CTCTATGCAG AACTTGGCAG TCATATTCGA CCTGCTGCTG GACTCTTATA 360

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257  GGACTGCCAG GGAGTTTGAC ACCAGCCCCG GGCTGAAGTG CCTGCTGAAG AAAGTGTCTG 420
258  GCATCGGGGG CGCCGCCAAC CTCTACCGCC AGTCTGCGAT GAGCTTTAAC ATTTATTTCC 480
259  ACGCCCTGGT GTGTGCTGTT CTCACCAATC AAGAAACCAT CACGGCCGAG CAAGTGAAGA 540
260  AGGTCCTTTT TGAGGACGAC GAGAGAAGCA CGGATTCTTC CCAGCAGTGT TCATCTGAGG 600
261  ATGAAGACAT CTTTGAGGAA ACCGCCCAGG TCAGCCCCCC GAGAGGCAAG GAGAAGAGAC 660
262  AGTGGCGGGC ACGGATGCCC TTGCTCAGCG TCCAGCCTGT CAGCAACGCA GATTGGGTGT 720
263  GGCTGGTCAA GAGGCTGCAC AAGCTGTGCA TGGAAGTGTG CAACAACACT ATCCAGATGC 780
264  ACTTGACCTT GGAGAACTGT ATGGAGGAGC CTCCCATCTT CAAGGGCGAC CCGTTCTTCA 840
265  TCCTGCCCTC CTTCCAGTCC GAGTCATCCA CCCCATCCAC CGGGGGCTTC TCTGGGAAAG 900
266  AAACCCCTTC CGAGGATGAC AGAAGCCAGT CCCGGGAGCA CATGGGCGAG TCCCTGAGCC 960
267  TGAAGGCCGG TGGTGGGGAC CTGCTGCTGC CCCCAGCCC CAAAGTGGAG AAGAAGGATC 1020
268  CCAGCCGGAA GAAGGAGTGG TGGGAGAATG CGGGGAACAA AATCTACACC ATGGCAGCCG 1080
269  ACAAGACCAT TTCAAAGTTG ATGACCGAAT ACAAAAAGAG GAAACAGCAG CACAACCTGT 1140
270  CCGCGTTCCC CAAAGAGGTC AAAGTGGAGA AGAAAGGAGA GCCACTGGGT CCCAGGGGCC 1200
271  AGGACTCCCC GCTGCTTCAG CGTCCCCAGC ACTTGATGGA CCAAGGGCAA ATGCGGCATT 1260
272  CCTTCAGCGC AGGCCCCGAG CTGCTGCGAC AGGACAAGAG GCCCCGCTCA GGCTCCACCG 1320
273  GGAGCTCCCT CAGTGTCTCG GTGAGAGACG CAGAAGCACA GATCCAGGCA TGGACCAACA 1380
274  TGGTGCTAAC AGTTCTCAAT CAGATTGAGA TTCTCCAGA CCAGACCTTC ACGGCCCTCC 1440
275  AGCCCGCAGT GTTCCCGTGC ATCAGTCAGC TGACCTGTCA CGTGACCGAC ATCAGAGTTC 1500
276  GCCAGGCTGT GAGGGAGTGG CTGGGCAGGG TGGGCCGTGT CTATGACATC ATTGTGTAGC 1560
277  CGACTCCTGT TCTACTCTCC CACCAAATAA CAGTAGTGAG GGTTAGAGTC CTGCCAATAC 1620
278  AGCTGTTGCA TTTTCCCCAC CACTAGCCCC ACTTAACTA CTACTACTGT CTCAGAGAAC 1680
279  AGTGTTCCTT AATGTAAAAA GCCTTTCCAA CCACTGATCA GCATTRGGGC CATACTAAGG 1740
280  TTTGTATCTA GATGACACAA ACGATATTCT GATTTTGCAC ATTATTATAG AAGAATCTAT 1800
281  AATCCTTGAT ATGTTTCTAA CTCTGAAAGT ATATTTCCCA GTGCTTTTGC TTACAGTGT 1860
282  GTCCCCAAAT GGGTCATTTT CAAGGATTAC TCATTTGAAA ACACTATATT GATCCATTTG 1920
283  ATCCATCATT TAAAAAATAA ATACAATTCC TAAGGCAATA TCTGCTGGTA AGTCAAGCTG 1980
284  ATAAACACTC AGACATCTAG TACCAGGGAT TATTAATTGG AGGAAGATTT ATGGTTATGG 2040
285  GTCTGGCTGG GAAGAAGACA ACTATAAATA CATATTCTTG GGTGTCATAA TCAAGA 2096
287 (2) INFORMATION FOR SEQ ID NO: 11:
289 (i) SEQUENCE CHARACTERISTICS:
290 (A) LENGTH: 68 base pairs
291 (B) TYPE: nucleic acid
292 (C) STRANDEDNESS: single
293 (D) TOPOLOGY: linear
296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
298 AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC 60
299 CGGGAATT 68
301 (2) INFORMATION FOR SEQ ID NO: 12:
303 (i) SEQUENCE CHARACTERISTICS:
304 (A) LENGTH: 68 base pairs
305 (B) TYPE: nucleic acid
306 (C) STRANDEDNESS: single
307 (D) TOPOLOGY: linear
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
312 AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG 60
313 GAATTCCG 68
315 (2) INFORMATION FOR SEQ ID NO: 13:
317 (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09991681.txt

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L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:19 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:39 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:40 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:16 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:17 M:259 W: Allowed number of lines exceeded, (i) APPLICANT:
L:505 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:584 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:603 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:622 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:641 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31